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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/866,248C

DATE: 07/16/2003

TIME: 08:05:33

Input Set : A:\57155A.txt

Output Set: N:\CRF4\07162003\I866248C.raw

5 <110> APPLICANT: Gerald, Christophe P.G.
7 Jones, Kenneth A.
9 Bonini, James A.
11 Borowsky, Beth
15 <120> TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
17 and Uses Thereof
21 <130> FILE REFERENCE: 1795/57155-A
C--> 25 <140> CURRENT APPLICATION NUMBER: US/09/866,248C
C--> 27 <141> CURRENT FILING DATE: 2001-05-25
31 <150> PRIOR APPLICATION NUMBER: 09/161,113
33 <151> PRIOR FILING DATE: 1998-09-25
37 <160> NUMBER OF SEQ ID NOS: 42
41 <170> SOFTWARE: PatentIn Ver. 2.0 - beta
45 <210> SEQ ID NO: 1
47 <211> LENGTH: 1410
49 <212> TYPE: DNA
51 <213> ORGANISM: Rattus norvegicus
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59 ggagcagaca gtatggaggc ggagccctcc cagcctccca acggcagctg gcccttgggt 120
61 cagaacggga gtgatgtgga gaccagcatg gcaaccagcc tcaccttctc ctctactac 180
63 caacactcct ctccggtggc agccatgttc atcgcgccct acgtgtcat ctctctctc 240
65 tgcattggtg gcaacaccct ggtctgtctc attgtgtctc agaaccggca catgcgcact 300
67 gtcaccaaca tgtttatcct caacctggcc gtcagcgacc tgctgggtgg catcttctgc 360
69 atgcccacaa cccttgtgga caaccttacc actggttggc cttttgacaa cgccacatgc 420
71 aagatgagcg gcttgggtgca gggcatgtcc gtgtctgcat cggttttcac actggtggcc 480
73 atcgctgtgg aaaggttccg ctgcatcggt caccctttcc gcgagaagct gacccttcgg 540
75 aaggcgctgt tcaccatcgc ggtgatctgg gctctggcgc tgctcatcat gtgtccctcg 600
77 gcggtcactc tgacagtcac ccgagaggag catcacttca tgctggatgc tcgtaaccgc 660
79 tcctaccgcg tctactcgtg ctgggaggcc tggcccgaga agggcatgcg caaggtctac 720
81 accgcggtgc tcttcgcgca catctacctg gtgcccgtgg cgctcatcgt agtgatgtac 780
83 gtgcgcatcg cgcgcaagct atgccaggcc cccggtcctg cgcgcgacac ggaggaggcg 840
85 gtggccgagg gtggccgcac ttcgcgcgtt agggcccgcg tgggtcacat gctggtcatg 900
87 gtggcgctct tcttcacggt gtcctggctg cactctggg tgctgctgct gctcatcgac 960
89 tatggggagc tgagcgagct gcaactgcac ctgctgtcgg tctacgcctt ccccttggca 1020
91 cactggctgg ccttcttcca cagcagcgcc aaccccatca tctacggcta cttcaacgag 1080
93 aacttcgcgc gcggttcca ggctgccttc cgtgcacagc tctgctggcc tccctgggcc 1140
95 gccacaagc aagcctactc ggagcggccc aaccgcctcc tgcgcaggcg ggtgggtgtg 1200
97 gacgtgcaac ccagcgactc cggcctgcca tcagagtctg gccccagcag cgggggtcca 1260
99 gggcctggcc ggctgccact gcgcaatggg cgtgtggccc atcaggatgg cccgggggaa 1320
101 gggccaggct gcaaccacat gccctcacc atcccgccct ggaacatttg aggtggtcca 1380
103 gagaaggagg ggccagtagt cctgtggccc 1410
107 <210> SEQ ID NO: 2

p.6
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111 <212> TYPE: PRT
113 <213> ORGANISM: Rattus norvegicus
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125 Gln Asn Gly Ser Asp Val Glu Thr Ser Met Ala Thr Ser Leu Thr Phe
127 20 25 30
131 Ser Ser Tyr Tyr Gln His Ser Ser Pro Val Ala Ala Met Phe Ile Ala
133 35 40 45
137 Ala Tyr Val Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val
139 50 55 60
143 Cys Phe Ile Val Leu Lys Asn Arg His Met Arg Thr Val Thr Asn Met
145 65 70 75 80
149 Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys
151 85 90 95
155 Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp
157 100 105 110
161 Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser
163 115 120 125
167 Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys
169 130 135 140
173 Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Phe
175 145 150 155 160
179 Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Ile Met Cys Pro Ser
181 165 170 175
185 Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Leu Asp
187 180 185 190
191 Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro
193 195 200 205
197 Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile
199 210 215 220
203 Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala
205 225 230 235 240
209 Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala
211 245 250 255
215 Val Ala Glu Gly Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His
217 260 265 270
221 Met Leu Val Met Val Ala Leu Phe Thr Leu Ser Trp Leu Pro Leu
223 275 280 285
227 Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln
229 290 295 300
233 Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala
235 305 310 315 320
239 Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu
241 325 330 335
245 Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp
247 340 345 350
251 Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg

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253          355          360          365
257 Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly
259          370          375          380
263 Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg
265 385          390          395          400
269 Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu
271          405          410          415
275 Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile
277          420          425          430
289 <210> SEQ ID NO: 3
291 <211> LENGTH: 200
293 <212> TYPE: DNA
295 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 3
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303 gccaccccggt ctacaaacct caccttctcc tctactatc agcacacctc cctgtggcg 120
305 gccatgttca ttgtggccta tgcgtcatc ttcctgctct gcatgggtgg caacaccctg 180
307 gtctgtttca tcgtgtcaa
311 <210> SEQ ID NO: 4
313 <211> LENGTH: 66
315 <212> TYPE: PRT
317 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 4
323 Glu Pro Ser Gln Pro Pro Asn Ser Ser Trp Pro Leu Ser Gln Asn Gly
325 1          5          10          15
329 Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe Ser Ser Tyr
331          20          25          30
335 Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val Ala Tyr Ala
337          35          40          45
341 Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val Cys Phe Ile
343          50          55          60
347 Val Leu
349 65
355 <210> SEQ ID NO: 5
357 <211> LENGTH: 1302
359 <212> TYPE: DNA
361 <213> ORGANISM: Homo sapiens
365 <400> SEQUENCE: 5
367 gccgacaggg ctgcgcggga gaggttcac atgaatgaga aatgggacac aaactcttca 60
369 gaaaactggc atcccatctg gaatgtcaat gacacaaagc atcatctgta ctcatatatt 120
371 aatattacct atgtgaacta ctatcttcac cagcctcaag tggcagcaat cttcattatt 180
373 tctacttttc tgatcttctt tttgtgcatg atgggaaata ctgtggtttg ctttattgta 240
375 atgaggaaca aacatatgca cacagtcact aatctcttca tcttaaacct ggccataagt 300
377 gatttactag ttggcatatt ctgcatgcct ataactgctc tggacaatat tatagcagga 360
379 tggccatttg gaaacacgat gtgcaagatc agtggattgg tccagggaat atctgtcgca 420
381 gcttcagtct ttacgttagt tgcaattgct gtagataggt tccagtgtgt ggtctaccct 480
383 tttaaaccaa agctcactat caagacagcg tttgtcatta ttatgatcat ctgggtccta 540
385 gccatcacca ttatgtctcc atctgcagta atgttacatg tgcaagaaga aaaatattac 600
387 cgagtgcgac tcaactccca gaataaaacc agtccagtct actggtgccg ggaagactgg 660

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389 ccaaatcagg aaatgaggaa gatctacacc actgtgctgt ttgccaacat ctacctggct 720
391 cccctctccc tcattgtcat catgtatgga aggattggaa ttctactctt cagggtcgca 780
393 gttcctcaca caggcaggaa gaaccaggag cagtggcacg tgggtgtccag gaagaagcag 840
395 aagatcatta agatgctcct gattgtggcc ctgcttttta ttctctcatg gctgcccctg 900
397 tggactctaa tgatgctctc agactacgct gacctttctc caaatgaact gcagatcatc 960
399 aacatctaca tctacccttt tgcacactgg ctggcattcg gcaacagcag tgtcaatccc 1020
401 atcattttatg gtttcttcaa cgagaatttc cgccgtgggt tccaagaagc tttccagctc 1080
403 cagctctgcc aaaaaagagc aaagcctatg gaagcttatg ccctaaaagc taaaagccat 1140
405 gtgctcataa acacatctaa tcagcttgct caggaatcta catttcaaaa ccctcatggg 1200
407 gaaaccttgc tttataggaa aagtgtgtaa aaacccaac aggaattagt gatggaagaa 1260
409 ttaaaagaaa ctactaacag cagtgagatt taaaagagc ta 1302

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413 <210> SEQ ID NO: 6

415 <211> LENGTH: 420

417 <212> TYPE: PRT

419 <213> ORGANISM: Homo sapiens

423 <400> SEQUENCE: 6

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427 1 5 10 15
431 Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
433 20 25 30
437 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
439 35 40 45
443 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
445 50 55 60
449 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
451 65 70 75 80
455 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
457 85 90 95
461 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
463 100 105 110
467 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
469 115 120 125
473 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
475 130 135 140
479 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
481 145 150 155 160
485 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
487 165 170 175
491 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
493 180 185 190
497 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
499 195 200 205
503 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
505 210 215 220
509 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
511 225 230 235 240
515 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
517 245 250 255
521 Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile

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523          260          265          270
527 Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
529          275          280          285
533 Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
535          290          295          300
539 Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
541 305          310          315          320
545 Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
547          325          330          335
551 Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
553          340          345          350
557 Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Ala Leu Lys Ala Lys
559          355          360          365
563 Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
565          370          375          380
569 Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
571 385          390          395          400
575 Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
577          405          410          415
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583          420
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591 <211> LENGTH: 1293
593 <212> TYPE: DNA
595 <213> ORGANISM: Homo sapiens
599 <400> SEQUENCE: 7
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603 aacactgagg ccaccccggc tacaaacctc accttctcct cctactatca gcacacctcc 120
605 cctgtggcgg ccatgttcat tgtggcctat gcgctcatct tctgtctctg catggtgggc 180
607 aacaccctgg tctgtttcat cgtgctcaag aaccggcaca tgcatactgt caccaacatg 240
609 ttcatcctca acctggctgt cagtgcctg ctggtgggca tcttctgcat gccaccacc 300
611 cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
613 ttggtgcagg gcatgtctgt gtcggcttcc gttttcacac tgggtggccat tgctgtggaa 420
615 aggttccgct gcatcgtgca ccctttccgc gagaagctga ccctgcggaa ggcgctcgtc 480
617 accatcgccg tcatctgggc cctggcgctg ctcatcatgt gtccctcggc cgtcacgctg 540
619 accgtcaccg gtgaggagca ccaattcatg gtggacgccc gcaaccgctc ctaccctctc 600
621 tactcctgct gggaggcctg gcccgagaag ggcagtcgca gggctctacac cactgtgctc 660
623 ttctcgcaca tctacctggc gccgctggcg ctcatcgtgg tcatgtacgc ccgcatcgcg 720
625 cgcaagctct gccaggcccc gggcccgccc cccggggcg aggaggctgc ggaccgcga 780
627 gcatcgcgcg gcagagcgcg cgtggtgcac atgctggtca tgggtggcgt gttcttcacg 840
629 ctgtcctggc tgccgctctg ggcgctgctg ctgctcatcg actacgggca gtcagcgcg 900
631 ccgcagctgc acctggtcac cgtctacgcc ttccccttcg cgcactggct ggccttcttc 960
633 aacagcagcg ccaaccccat catctacggc tacttcaacg agaacttccg ccgcggcttc 1020
635 caggccgctt tccgcgcccc cctctgcccc cgcccgctcg ggagccacaa ggaggcctac 1080
637 tccgagcggc ccggcgggct tctgcacagg cgggtcttcg tgggtggtgc gccagcgac 1140
639 tccgggctgc cctctgagtc gggccctagc agtggggccc ccaggcccgg ccgctctccc 1200
641 ctgcggaatg ggcggtggc tcaccacggc ttgccaggg aagggcctgg ctgctccac 1260
643 ctgcccctca ccattccagc ctgggatatc tga 1293
647 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\57155A.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 3,9,10,12,15,21
Seq#:10; N Pos. 3,6,14,15,17,18

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,3,5,7,9,11,13,15,17,19,21,23,25,27,29,31,33,35,37,39,41
Seq#:1; Line(s) 43,45,47,49,51,53,55,57,59,61,63,65,67,69,71,73,75,77,79,81
Seq#:1; Line(s) 83,85,87,89,91,93,95,97,99,101,103,105,107
Seq#:2; Line(s) 109,111,113,115,117,119,121,123,125,127,129,131,133,135,137
Seq#:2; Line(s) 139,141,143,145,147,149,151,153,155,157,159,161,163,165,167
Seq#:2; Line(s) 169,171,173,175,177,179,181,183,185,187,189,191,193,195,197
Seq#:2; Line(s) 199,201,203,205,207,209,211,213,215,217,219,221,223,225,227
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Seq#:3; Line(s) 291,293,295,297,299,301,303,305,307,309,311
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Seq#:4; Line(s) 343,345,347,349,351,353,355
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Seq#:24; Line(s) 1169,1171,1173,1175,1177,1179,1181,1183,1185,1187,1189
Seq#:25; Line(s) 1191,1193,1195,1197,1199,1201,1203,1205,1207,1209,1211
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